ACCESS DB # 15365
PLEASE PRINT CLEARLY

Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: Art Unit: 163 Location (Bldg/Room#): ***********************************	Phone Number: 2- 076	xaminer # : 77512—Date: 5-17107 Serial Number: 09 1486,757 ults Format Preferred (circle): PAPBR DISK ***********************************
	•	·
To ensure an efficient and quality	~	sheet, claims, and abstract or fill out the following:
Title of Invention:	agtochore	1 CESO reductions
Inventors (please provide full	names): WITCHA	N et d'
-		B(V
Earliest Priority Date:	7/3/00	$\mathcal{O}_{\mathcal{N}_{\mathcal{N}}}$
alacted species or structures, keywo	t of the search topic, and describe as specific ords, synonyms, acronyms, and registry num special meaning. Give examples or relevant	cally as possible the subject matter to be searched. Include the abers, and combine with the concept or utility of the invention. t citations, authors, etc., if known.
For Sequence Searches Only Pappropriate serial number.	lease include all pertinent information (pare	ent, child, divisional, or issued patent numbers) along with the
	Please Send	e Seg ID No: 10
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STAFF USE ONLY	Type of Search	Vendors and cost where applicable
Searcher:	NA Sequence (#)	STNDialog
Searcher Phone #:	AA Sequence (#)	Questel/OrbitLexis/Nexis
Searcher Location:	Structure (#)	Westlaw WWW/Internet
Date Searcher Picked Up: 3/20	Bibliographic	(1) In-house sequence systems
Date Completed:	Litigation	Commercial Oligomer Score/Length Interference SPDI Encode/Transl Other (specify)
Searcher Prep & Review Time:	Fulltext	

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
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2649
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12172.472 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45554873 seqs, 20411521753 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
ptodata/1/pna/US097A_COMB.seq:
                                                                                                                                                                                                                                                                                            1/pna/US084 COMB.seq:*
1/pna/US085 COMB.seq:*
1/pna/US085 COMB.seq:*
1/pna/US086 COMB.seq:*
1/pna/US086 COMB.seq:*
1/pna/US088 COMB.seq:*
1/pna/US089 COMB.seq:*
1/pna/US089 COMB.seq:*
1/pna/US090 COMB.seq:*
                                                                          1/pna/US095C_COMB.seq:*
1/pna/US095D_COMB.seq:*
1/pna/US096A_COMB.seq:*
1/pna/US096B_COMB.seq:*
                                                                                                                                                         l/pna/US093B_COMB.seq:*
l/pna/US094_COMB.seq:*
l/pna/US095A_COMB.seq:*
l/pna/US095B_COMB.seq:*
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pna/US093B_COMB.seq:
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44. 44. 46. /cgm2_6/ptodata/1/pna/US099F_COMB.seq; *
46. /cgm2_6/ptodata/1/pna/US099F_COMB.seq; *
47. /cgm2_6/ptodata/1/pna/US1003_COMB.seq; *
48. /cgm2_6/ptodata/1/pna/US1003_COMB.seq; *
49. /cgm2_6/ptodata/1/pna/US101A_COMB.seq; *
50. /cgm2_6/ptodata/1/pna/US101A_COMB.seq; *
51. /cgm2_6/ptodata/1/pna/US101A_COMB.seq; *
52. /cgm2_6/ptodata/1/pna/US101A_COMB.seq; *
53. /cgm2_6/ptodata/1/pna/US101A_COMB.seq; *
54. /cgm2_6/ptodata/1/pna/US101A_COMB.seq; *
55. /cgm2_6/ptodata/1/pna/US101A_COMB.seq; *
56. /cgm2_6/ptodata/1/pna/US101A_COMB.seq; *
57. /cgm2_6/ptodata/1/pna/US101A_COMB.seq; *
67. /cgm2_6/ptodata/1/pna/US101A_COMB.seq; *
68. /cgm2_6/ptodata/1/pna/US107A_COMB.seq; *
68. /cgm2_6/ptodata/1/pna/US107B_COMB.seq; *
68. /cgm2_6/ptodata/1/pna/US107B_COMB.seq; *
68. /cgm2_6/ptodata/1/pna/US107B_COMB.seq; *
69. /cgm2_6/p
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 22, 2005, 05:22:02; Search time 760 Seconds (without alignments) 7754.887 Million cell updates/sec

Title: Perfect score: Sequence:

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

11689648 seqs, 1112441377 residues

Total number of hits satisfying chosen parameters: 23379296

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pending_Patents_NA_New:*

Database :

/cgm2_6/ptodata/1/pna/US10_NEW_COMB.seq4:*
/cgm2_6/ptodata/1/pna/US11_NEW_COMB.seq2:*
/cgm2_6/ptodata/1/pna/US11_NEW_COMB.seq2:*
/cgm2_6/ptodata/1/pna/US11_NEW_COMB.seq3:*
/cgm2_6/ptodata/1/pna/US60_NEW_COMB.seq3:*

Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and 18 derived by analysis of the total score distribution.

SUMMARIES

Regult No.

Query
Score Match Length no in

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compagen Ltd.

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       May 22, 2005, 08:25:35 ; Search time 1432 Seconds (without alignments)
11343.938 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published Applications NA: *
[6/ptodata/1/pubpna/US10E_PUBCOMB.seq:6/ptodata/1/pubpna/US10F_PUBCOMB.seq:6/ptodata/1/pubpna/US10F_PUBCOMB.seq:6/ptodata/1/pubpna/US11_NEW_PUB.seq:*6/ptodata/1/pubpna/US11_NEW_PUB.seq:*6/ptodata/1/pubpna/US60_NEW_PUB.seq:*6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
                                                                                                                                                    /pubpna/US09C_PUBCOMB.seq:*
/pubpna/US09_NEW_PUB.seq:*
/pubpna/US10A_PUBCOMB.seq:*
/pubpna/US10B_PUBCOMB.seq:*
/pubpna/US10C_PUBCOMB.seq:*
/pubpna/US10C_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                        nubpna/US06_FUBCOMB.seq:*
nubpna/US07_NEW_PUB.seq:*
nubpna/PCTUS_PUBCOMB.seq:
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/US09B_PUBCOMB.seq:*
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                                                                                                                                                                                                                                                                                                         NEW PUB. seq: *
PUBCOMB. seq: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query
No. Score Match Length DB ID

Description

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
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Total number of hits satisfying chosen parameters: 2405568

1202784 seqs, 818138359 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : Issued_Patents_NA:*

18sued_Patents NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query
No. Score Match Length DB ID

Description

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

Title: Perfect score: Sequence: Database : Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0
Maximum DB seq length: 2000000000 Total number of hits satisfying chosen parameters: Searched: Scoring table: OM nucleic - nucleic search, using sw model Run on: May 22, 2005, 00:44:41 ; Search time 1305 Seconds (without alignments)
12016.394 Million cell updates/sec 4390206 seqs, 2959870667 residues Gapop 10.0 , Gapext 1.0 US-09-486-757-10 2649 N_Geneseq_16Dec04:* 1: geneseqn1980s:* geneseqn1980s:*
geneseqn1990s:*
geneseqn2000s:*
geneseqn2001as:* geneseqn2003bs:*
geneseqn2003cs:*
geneseqn2003ds:*
geneseqn2004as:*
geneseqn2004bs:* geneseqn2002bs:*
geneseqn2003as:* geneseqn2001bs: * 8780412

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                            1039
1030.8
997.2
994.6
987.6
                                                                                                                                  1104.8
1094.8
1086.2
1071.6
1061.4
                                                                                                                                                                                            2645.8
1126.4
                                                       985
969.8
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                                                                                                                                                                                                                               Match Length DB
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GenEmbl: *
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Copyright (c) 1993 - 2005 Compugen Ltd.
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gb_vi:*
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AY170374
AB086169
BT013756
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AF302496
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       AY520902 Hypericum
AY054688 Arabidops
BT008426 Arabidops
X66016 A.thaliana
A75959 Sequence 1
U67186 Eschscholtz
AF302497 Hybrid po
Z49767 Pseudoctsuga
AF302498 Hybrid po
AX506108 Sequence
                                                                                                                                                                     U67185 Papaver som
AF302496 Hybrid po
L07843 Vigna radia
Z26252 V.sativa mR
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                                                                                                                                     13756 Lycopersi
                                                                                                                                              0374 Glycine m
6169 Ophiorrhi
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282.4	295.8	•	569.6	586.4		659.2	807.6	807.6	807.6	807.6	807.6	808.4	808.4	850	852.6	859.8	862.4	864.8	867.4	873.6	874	875	875	875.2	895.4
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1078	715	1023	2312	2016	1714	1539	1863	1863	1863	1863	1863	2298	2298	2420	2482	2112	2545	2472	2333	2618	2466	2423	2290	.2556	2136
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PAB132538	HTU58629	AY059162	AF367288	AX654074	AK101320	HTL2NFR	HTU2NFR	AX370663	AX082548	AR282641	AR205034	AK099083	AK068915	TAE303373	AK102060	A75963	AF002698	AY532374	AF123610	CRCPRA	AF024634	A75961	ATATR2M	AF024635	AF325101
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AJ132538 Picea abi	Φ	AY059162 Arabidops			AK101320 Oryza sat	Z26251 H.tuberosus	Z26250 H.tuberosus	AX370663 Sequence	AX082548 Sequence		AR205034 Sequence	AK099083 Oryza sat	AK068915 Oryza sat	AJ303373 Triticum		A75963 Sequence 5	AF002698 Pisum sat	AY532374 Ammi maju	AF123610 Triticum		AF024634 Petroseli	A75961 Sequence 3	X66017 A.thaliana	AF024635 Petroseli	AF325101 Arabidops

ALIGNMENTS

source	FEATURES		JOURNAL	TITLE	AUTHORS	REFERENCE	PUBMED	MEDLINE	JOURNAL		TITLE	AUTHORS	REFERENCE				ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	PSU67185	RESULT 1
12650	Location/Qualifiers	Universitaet Muenchen, Karlstrasse 29, Munich 80333, Germany	Submitted (19-AUG-1996) Laboratorium fuer Molekulare Biologie,	Direct Submission	Rosco, A. and Kutchan, T.M.	2 (bases 1 to 2650)	9434750	98096363	Arch. Biochem. Biophys. 348 (2), 369-377 (1997)	reductases from the Papaveraceae	Cloning and heterologous expression of NADPH-cytochrome P450	Rosco, A., Pauli, H.H., Priesner, W. and Kutchan, T.M.	1 (bases 1 to 2650)	Papaveraceae; Papaver.	Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Papaver somniferum	Papaver somniferum (opium poppy)	•	U67185.1 GI:2580496	U67185	complete cds.	Papaver somniferum NADPH:ferrihemoprotein oxidoreductase mRNA,	PSU67185 2650 bp mRNA linear PLN 06-MAR-1998		

SGS

/organism="Papaver somniferum" /mol_type="mRNA" /db_xref="taxon:3469"

note="cell suspension culture"

/BC_number="1.6.2.4"
/function="catalyzes the reduction of the
heme-thiolate-dependent monooxygenases and oxidases;
reduces cytochrome c"

/codon_start=1 /product="NaDDH:ferrihemoprotein oxidoreductase" /protein_id="AAC05021.1" /db_xref="GI:2580497"

note="cytochrome P-450 reductase"

translation="MGSNNLANSIESMLGISIGSEYISDPIFIMVTTVASMLIGFGFF"

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781 GATGATTTTACTGCTTGGCGAGAATTGTTGGGACTGAATTGGATCAGTTGCTCAAAGAT 840	721 AAACAAGGTGCAAAGCGCATTGTTCAAGTGGGGGCTCGGTGACGATGATCAATGCATTGAA 780	661 GGTAACCGTCAATACGAGCATTTCAACAAGATCGCGGTAGATGTGGATGAGCAACTCGGT 720	601 ACTCAGGAACATGAAAGGGGAGAGTGGCTTCAGCAACTAACT	541 GTAGCCACTTATGGTGATGGTGAGCCAACTGACAATGCTGCGAGATTTTACAAATGGTTC 600 	481 GCAGCCGAGGATGATCAATATGAAGAGAAATTAAAGAAAG	421 GANGAAATTAAGGCAAAGTACAAGAAAGCAGTTGTTAAAGTAGTTGACCTGGATGACTAT 480 	361 CTCACTATATTTTTTGGTACTCAGACTGGTACTGCTGAAGGATTTGCTAAGGCATTGGCA 420	301 TATAAACCAATAATTGATAAAGAAGAAGAAGATGAAGTTGAAGTTGATCCTGGTAAAATTAAG 360 	241 GGATTTGGTTTCTTCGCATGTATGAAATCTTCGTCTTCTCAATCAA	181 TCAGAATATATTTCTGACCCAATTTTCATTATGGTCACAACTGTAGCTTCAATGCTGAIT 240 	121 ATTATGGGTTCGAATAATTTAGCTAATTCGATTGAATCGATGTTAGGAATATCAATAGGA 180 	61 CGAATCTACTTGAAATACATTCGATTGCTTCTCTCTGTTTAAGCTTCAGAGTCTCTGCTA 120	1 CGGCACGAGCTTGTTAGTATCTTCTAGGGTTTGAAAAGAAGCACAGĞGAGAAGCAAAAGT 60 	Query Match 99.9%; Score 2645.8; DB 8; Length 2650; Best Local Similarity 99.9%; Pred. No. 0; Matches 2647; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	AVPODSWAPI FVRTSNEKLPADDSTPII MVGPCTGLAPPRGPLQERMALKENGAQLGP AVLFFGCRNRNMDFI YEDBLINNFVERGVI SELVI AFSREGEKKEYVOHKOMEKATDVW NVI SGDGYL YVCGDAKGMARDVHRTLHTI AQEQGPMESSAAEAAVKKLQVEERYLRDV W"	ANGDVAFDILHPCRTIVAQQRELHKFKSDRSCIHLEFDISGSSLTYETGDHVGVYAEN CDETVEEAGKLLGQFLDLLFSJHTDKEDGSSPGSSSLEPFFGFCTLAGALARYADLLN PPRKASLIALSAHASVPSEARRLFRISSPLGKNEVSKOVGSGRSLLEIMAEFPSAKF PRKASLIALSAHASVFSTALSTALSTALSTALSTALSTALSTALSTALSTALSTAL	ACMKSSSSOSKDIETYKPIIDKEEEEIEVDPGKIKLTIFFGTOTGTAEGFAKALAEEI KAKYKKAVVKVVDLDDYAAEDDQYEEKLKKESLVFFMVATYGDGEPTDNAARFYKWFT QEHERGEWLQQLTYGVFGLGNRQYEHFMKIAVDVDEQLGKQGAKRIVQVGLGDDDQCI GDDFTANRELLWTELGOLKKDGDAAPSVTATFYTATVTHETYAALDDKHINT
																	
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                            1 (bases 1 to 2498)
Ro,D.K., Ehlting, J. and Douglas, C.J.
Ro,D.K., Ehlting, J. and Douglas, C.J.
Cloning, Functional Expression, and Subcellular Localization
Multiple NADPH-Cytochrome P450 Reductases from Hybrid Poplar
Plant Physiol. 130 (4), 1837-1851 (2002)
                                                                                                          Populus balsamifera subsp. trichocarpa x Populus deltoides Populus balsamifera subsp. trichocarpa x Populus deltoides Populus balsamifera subsp. trichocarpa x Populus deltoides Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Epermatophyta; Magnollophyta; eudicotyledons; core eudicots; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Salicaceae; Salicacea; Populus.
                                                                                                                                                                                                                                           AF302496 2498 bp mRNA linear Hybrid poplar (Populus trichocarpa x P. deltoides) P450 oxydoreductase isoform 1 mRNA, complete cds.
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ACTAACTTATGGTGTTTTTGGGTAACCGTCAATACGAGCATTTCAACAAGATCGC

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Best Local Similarity
Matches 1517; Conserv
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Direct Submission
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